

M A S L D R V K V L V L G D S
 AGGGAAGGCAGTGGCAAG ATG GCG TCC CTG GAT CGG GTG AAG GTA CTG GTG TTG GGA GAC TCA SEQ ID NO:2
 ↑SEQ ID NO:3↓
 G V G K S S L V H L L C Q N Q V L G N F 35
 GGT GTT GGG AAA TCT TCG TTA GTC CAT CTC CTA TGC CAA AAT CAA GTG CTG GGA AAT CCA 105
 S W T V G C S V D V R V H D Y K E G T F 55
 TCA TGG ACT GTG GGC TGC TCA GTG GAT GTC AGA GTT CAT GAT TAC AAA GAA GGA ACC CCA 165
 E E K T Y Y I E L W D V G G S V G S A S 75
 GAA GAG AAG ACC TAC TAC ACA GAA TTA TGG GAT GTT GGA GGC TCT GTG GGC AGT GCC AGC 225
 S V K S T R A V F Y N S V N G I I F V H 95
 AGC GTG AAA AGC ACA AGA GCA GTA TTC TAC AAC TCC GTA AAT GGT ATT ATT TTC GTA CAC 285
 D L T N K K S S Q N L R R W S L E A L N 115
 GAC TTA ACA AAT AAG AAG TCC TCC CAA AAC TTG CGT CGT TGG TCA TTG GAA GCT CTC AAC 345
 R D L V P T G V L V T N G D Y D Q E Q F 135
 AGG GAT TTG GTG CCA ACT GGA GTC TTG GTG ACA AAT GGG GAT TAT GAT CAA GAA CAG TTT 405
 A D N Q I P L L V I G T K L D Q I H E T 155
 GCT GAT AAC CAA ATA CCA CTG TTG GTA ATA GGG ACT AAA CTG GAC CAG ATT CAT GAA ACA 465
 K R H E V L T R T A F L A E D F N P E E 175
 AAG CGC CAT GAA GTT TTA ACT AGG ACT GCT TTC CTG GCT GAG GAT TTC AAT CCA GAA GAA 525
 I N L D C T N P R Y L A A G S S N A V K 195
 ATT AAT TTG GAC TGC ACA AAT CCA CGG TAC TTA GCT GCA GGT TCT TCC AAT GCT GTC AAG 585
 L S R F F D K V I E K R Y F L R E G N Q 215
 CTC AGT AGG TTT TTT GAT AAG GTC ATA GAG AAG AGA TAC TTT TTA AGA GAA GGT AAT CAG 645
 I P G F P D R K R F G A G T L K S L H Y 235
 ATT CCA GGC TTT CCT GAT CGG AAA AGA TTT GGG GCA GGA ACA TTA AAG AGC CTT CAT TAT 705
 D 237
 GAC TGA 711
 ←SEQ ID NO:3↑
 ATTACACTCATCCTTTGGAAGAGTGAGCAAGCAGTGGCAGTTTTTCACAGCTCATCTTGCTGTGTTCATTATTACCAT
 CACAGCCTTTTAACAAAATCATCTTAAATGCTACCCCTTACGCCTTACCCCTTAATGGAAAAATGAAAGGAAGTGACAA
 TACGGGAGGTCCAAACTTTGTCCCTGTTCTCTGTGTTCCTTACCTTCTGTCCCTGTGTATAGATTATGTAAAGCCTT
 GTGTAAATATGAGATGTTGTCAAAATGATGCAGTAAATGAGCAATGACAGTGTACTGCAGAGAAAATTTACTCTTGCCT
 AGAACTGGAGGGTTTTATGGGTCTGTAATTTTCCACACTCATTGCTGAAAGCTTAATTAAGTACTTCAAAAACGTAT
 CTCCATTGTTTTACCTTCTTGAGGGGAACGGTCTGTGTTAACCAGCCCTGAGTTGTCTACCCCAACAACTCTCTGTCAAT
 TTCAAAGATGCAPAAATGGTGTATTTAATTGTCTCCACCATTGTACACACAGGAATGCCTAATAATAGCAACCCCTTGT
 CTCCCTCTCTCTCTCTTTGCAATGGCTCAGTGACTGGAAGAGCGGACTAATAGCCAGAGTTAAATATAAATACAAAT

FIG. 1A

TAATAATACATAGAGAACAGCAATACCAGAAAAAGAATTCTGGTAAATGATGTGAAAAATTGACAGCTCCCTCACT
CTTAAGGTTGCTGCTATATACAGTCTAGGTTTTCTGTTTGGAAATAGGTAGGGTAAATCTAAGACCTGCACAAGGGCA
GTGAGAGACATTTACAGCCTCCTCTCTATTGTTTTTTAAGGAAAAGTCAACTCCTGAAATGTCCCTTAGCTATAATC
AGAAACTAAGAATATTATTCTGTGTCAACAATGTATTTATGGAGAGAAGTAAAAATAAGTTCCACAGCAACACAAAAA
CATGAATTATTGAACTA

0045473.003400

107253 E2F5H660

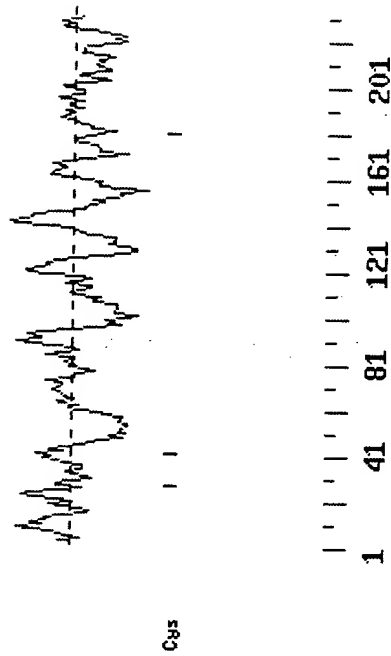


FIG. 2

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*->GlgflkiflklglwnKEmRILiLGLDnAGKTTILykLklge.ivtt SEQ ID NO:4
      ++l +    +++L+LG + GK+ +++ L +++ + +
47324  2  -----ASLDR---VKVLVLGDSGVGKSSLVHLLCQNQvLGNP 35
      iPTiGFNVetveykN.....ikFtvWDvGGQ.....eslRPlW
      + T+G v + + ++++++++ + WdvGG ++ ++ +s R +
47324  36 SWTVGCSV-DVRVHDykegtpeektYYIELWDVGGsvgsassvKSTRAV- 83
      rnYfpnTdavIfVDSaDreRieeakeELhaLLneeeL.....
      + +++++IfV D ++ + + L + e +++ +++ ++
47324  84 --FYNSVNGIIFVHDLTNKK---SSQNLRRWSLEALNrdlvptgvlvtn 127
      .....adAplLifANKQDlpgAmseaEi...reaLgLhelksgskg
      ++ +++++ + plL+ + K D + +E+ +++ L +
47324  128 gdydqeqlfADNQIPLLVIGTKLDQIHETKRHEVltrTAFLAEDFNP-E-- 174
      kVtl.e.gdRpWeiaggcsAvkGeGLyEGldWLSnnikkr<-*
      ++ l+ ++ R + ++Avk l + + +++++
47324  175 EINLdCtNPRYLAAGSSNAVK-----LSRFFDKVIEK 206

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FIG. 3

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*->KlVliGDsGVGKSsLliRfTdnkFveeYipTIGvDFytktevD... SEQ ID NO:5
      K++++GDsGVGKSsL++ +n+ T+G+ ++ ++ +++
47324  8  KVLVLGDSGVGKSSLVHLLCQNQVLGNPSWTVGCSVDVRVHDYKegt 54
      ..GktvkLqIWDTAGQERFralrpa.....YYRgAqGfLLVYDITs
      ++ kt+ ++WD G ++ +a++ +++++ +Y +G++ V D T+
47324  55 peEKTYYYIELWDVGG-----SVGSAssvkstravFYNSVNGIIFVHDLTN 99
      rdSFenvkkWleeilr..had.....kdenvpivLVGNKc
      ++S +n+++W e l+++ +++ +++++ +++++ d+ +p + +G+K
47324  100 KKSSQNLRRWSLEALNrdLVPTgvlvtngdydqeqlfADNQIPLLVIGTKL 149
      DLeddedlelte.gqkRvVsteeGealAkelgA.....lpFmETSA
      D + e++ +V t ++ lA++++ ++ + + + + +
47324  150 DQIH-----EtKR-HEVLTRTAF-LAEDFNPeiinldctnPRYLAAGS 190
      KtntNVeeaeFeelareilkkvsevnvnlldqpakkkkkskCcil<-*
      +++ F+ +++++ + +++++++ + +k+ +
47324  191 SNAVKLSRFFDKVIEKRYFLREGNQIPGPPD-RKRFGAGTLK 231

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FIG. 4

47324-381552003500

Query: 35 PSWTV-GCSVDVRVHDYKEGTPEEKT--YYIELWDXXXXXXXXXXXXXTRAVFYNSVNGI 91
 P+WT S D + Y TP Y++E +D R FY +++GI
 Sbjet: 69 PTWTTTPSSSEDSENYPYMRSTPTTTNILYFVEFYDLNSDWRMCRQQ---RESFYKNIDGI 125 SEQ ID
 NO:6

Query: 92 IFVHDLTNKKSSQNLRRWSLEALNRDLVPTGVLVTNGDYDQEQFADNQIPLLIVIGTKLDQ 151
 + V+++ S +L W + L + + + + P+LV+GT LD+
 Sbjet: 126 VLVYNMLELSSQDSLHDWLYDPLRQICKHRHLRI-----RSILKNHNAPILVVGNTLNDK 179

Query: 152 IHETKRHEVLTRTAFLAEDFNPEEINLDCTNPRYLAAGSSNAVKLSRFFDKVIE-KRYF 209
 + L R +A N EE+ ++C +P+ S N KL F ++VIE K F
 Sbjet: 180 L---MRRPLRRRGSIAHQNLNVEEMLVNCCLDPQSFVDKSRNQGLYGLNRVIEFKEQF 234

FIG. 5a

Query: 7 VKVLVLGDSGVGKSSLVHLLCQNVLGPN-SWTVG---CSVDVRVHDYKE 52
 V++L+LGD GVGK+SL +L+ ++ P S TVG V VR+H+Y +
 Sbjet: 12 VRILMLGDRGVGKTSLTNLMATTEITPTPDSRTVGEESWHVQVRLHEYSK 61 SEQ ID NO:7

FIG. 5b

Query: 121 TGVLVTNGD--YDQEQFAD-NQIPLLIVIGTKLDQIHETKRHEVL--TRTAFLAEDFNPEE 175
 T L T+G +D E+F Q P+LV+GTKLD + E KRH + + +A+ EE
 Sbjet: 19 TDNLGTDGHILFDMEEFLGATQTPILVMGTKLDLLDE-KRHPKMGVKKPGGIADKCGAEE 77 SEQ ID
 NO:8

Query: 176 INLDCTNPRYLAAGSSNAVKLSRFFDKVIEKRYFLR-----EGNQIPGFPDRKRFGAG 228
 I L+C N R LAAG+++AVKLSRFFD+VIE R LR + PDR+RFG
 Sbjet: 78 IWLNCNRSRLAAGTTDAVKLSRFFDRVIENRKALRAALAFGVSSSNVSPDRRRFGPT 137

Query: 229 TLK 231
 + K
 Sbjet: 138 SAK 140

FIG. 6

FIG. 5a

Query: 6 RVKVLVLGDSGVGKSSLVHLLCQNQVLGNPSWTVGCSVDVRVHDYKEGTPEEKTYIE 63
+V+VLV+GDSGVGK+SLVHL+ + + P T+GC+V V+ Y G+P + I+
Sbjct: 80 QVRVLVVGDSGVGKTSLVHLINKGSSIVRPPQTIGCTVGVKHITY--GSPASSSSSIQ 135 SEQ ID NO:9

FIG. 7

Query: 8 KVLVLGDSGVGKSSLVHLL--CQNQ-----VLGNPSWTVGCSVDVRVHDYKEGT 54
K++++GDSGVGK+SL++ L +N V+ + T+G +V+ T
Sbjct: 7 KIVIIGDSGVGKTSLLNKLRFTEENSFTEEDPTTTRTVVDSYKSTIGVDFNVKTTIEVVD 66 SEQ ID
NO:10

Query: 55 PEEKTYIIELDWXXXXXXXXXXXXXTRAVFNSVNGIIFVHDLTNKKSS-QNLRRWSLEA 113
+ K +++WD A +Y I V+D+ + +SS +N +W E
Sbjct: 67 -DGKNIKLQIWDTAGQERYRSMLEA-YRGAEADIIVDVDSSESSFENQTKWLKEI 124

Query: 114 LNRDLVPTGVLVTNGDYDQEQFADNQIPLLVIGTKLD-QI---HETKRHEVLTRTAFLAE 169
L +N E+ ++N +P+++G K D ++ E + + T A+
Sbjct: 125 LRH-----ASN-----EEASEN-VPIILVGNKADLEVPNPPEVEEEKEEASTEEEAQ 170

Query: 170 DFNPEEINLDCTNPRYLAAGSSNAVKLSRFFDKVIEKRYFLREGNQIPGFPDRKRF 225
F EE L P + + + F +++ R L++ +I D++++
Sbjct: 171 SF-AEEKGLGVV-PFIETSAKTTGTNVEEVFQELV--REILKKKKEIQEKADQEKY 222

FIG. 8

FIG. 7